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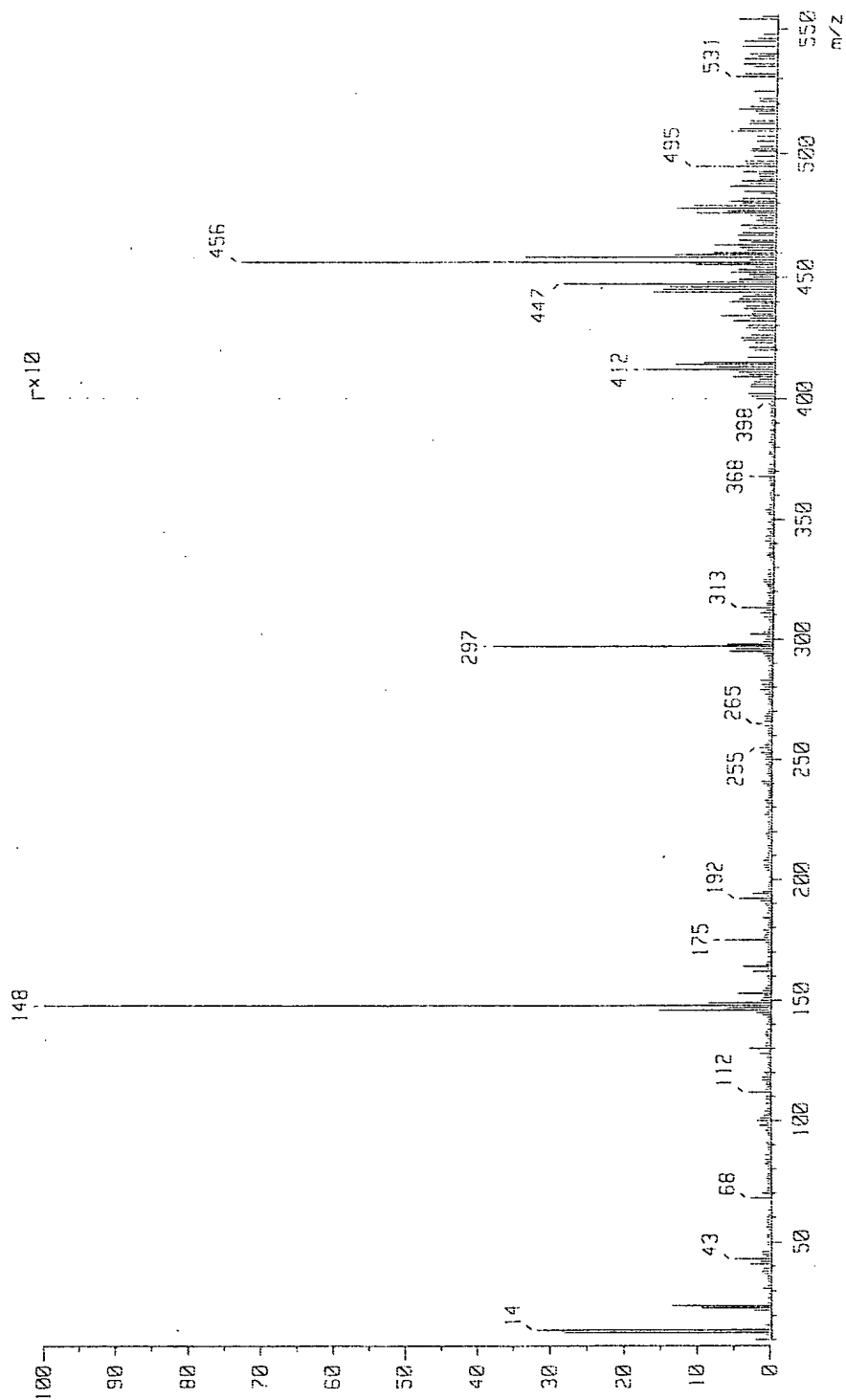
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Fig. 1



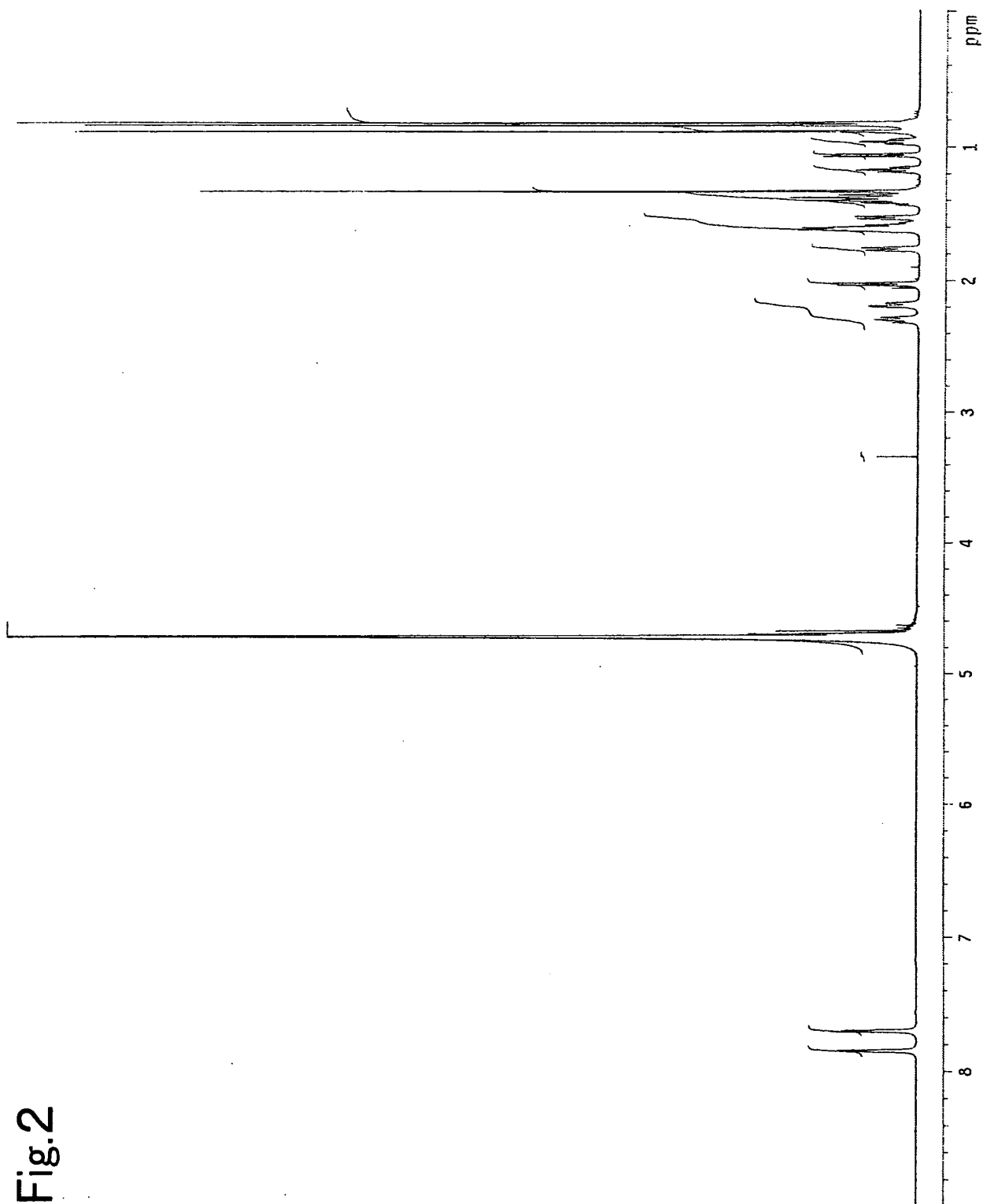
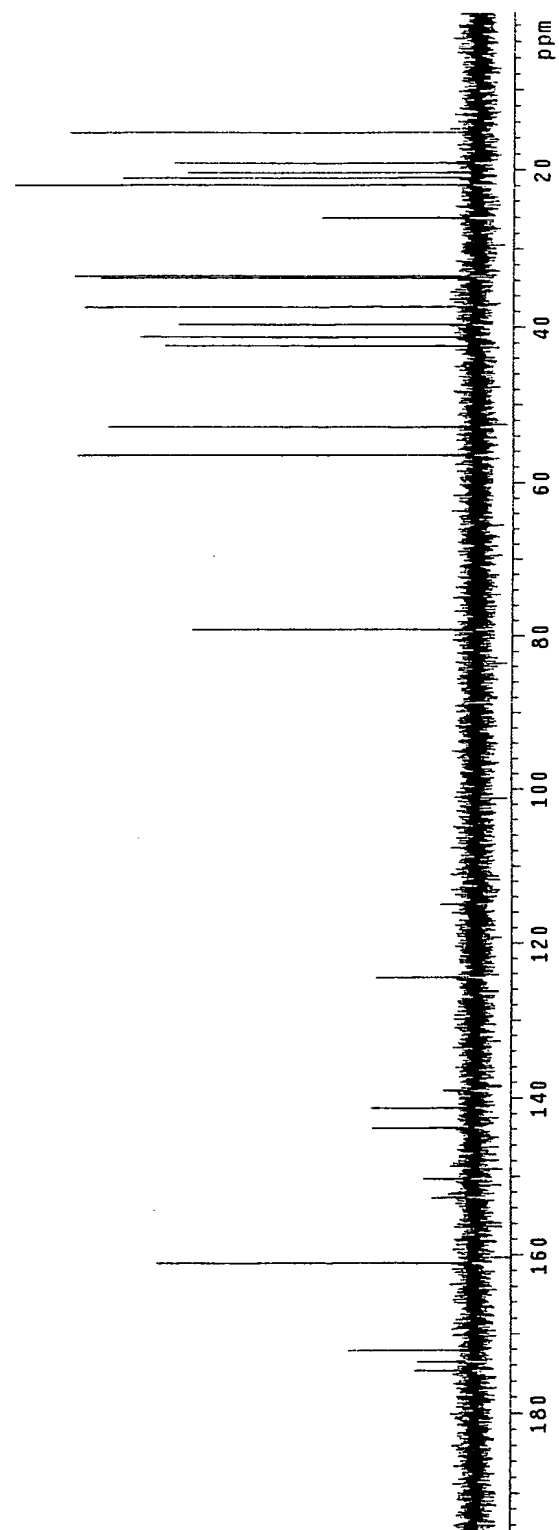
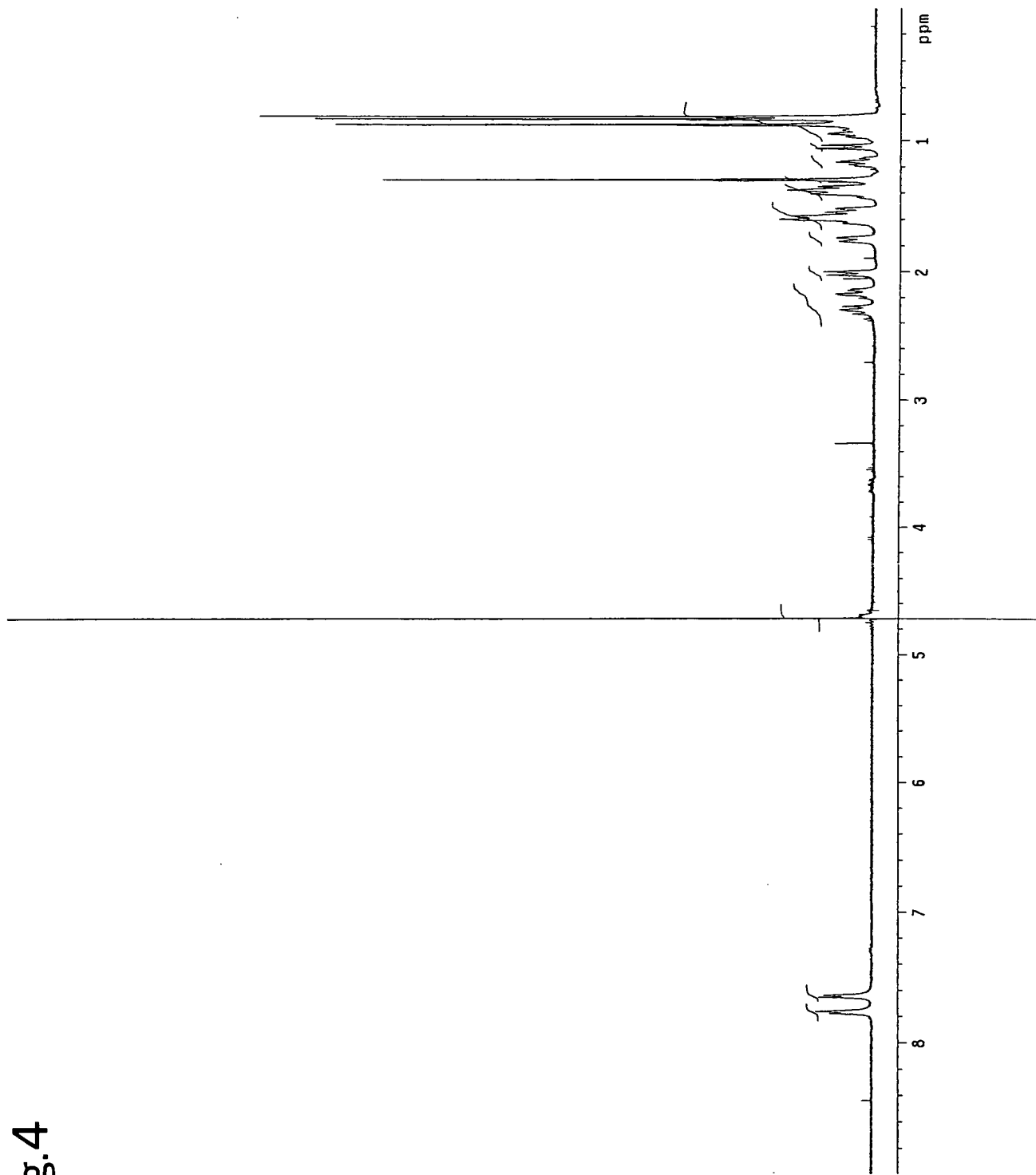


Fig.2

Fig.3





Fi. 4

Fig.5

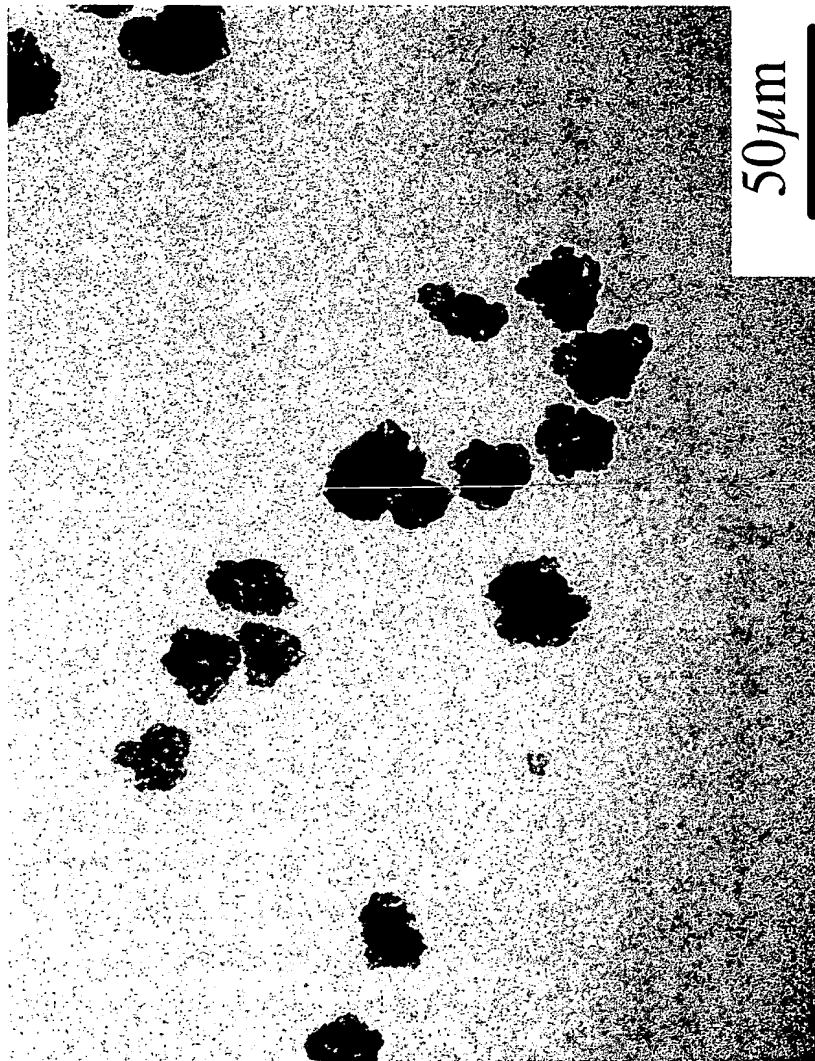
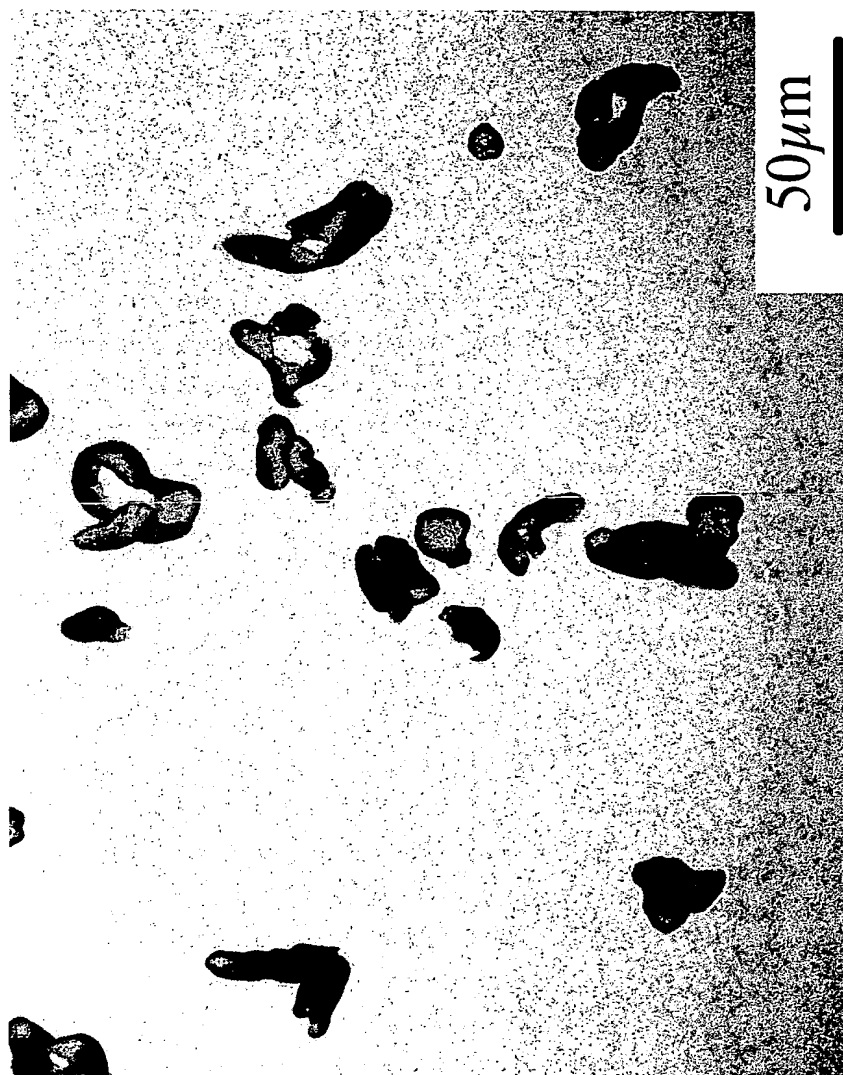


Fig.6



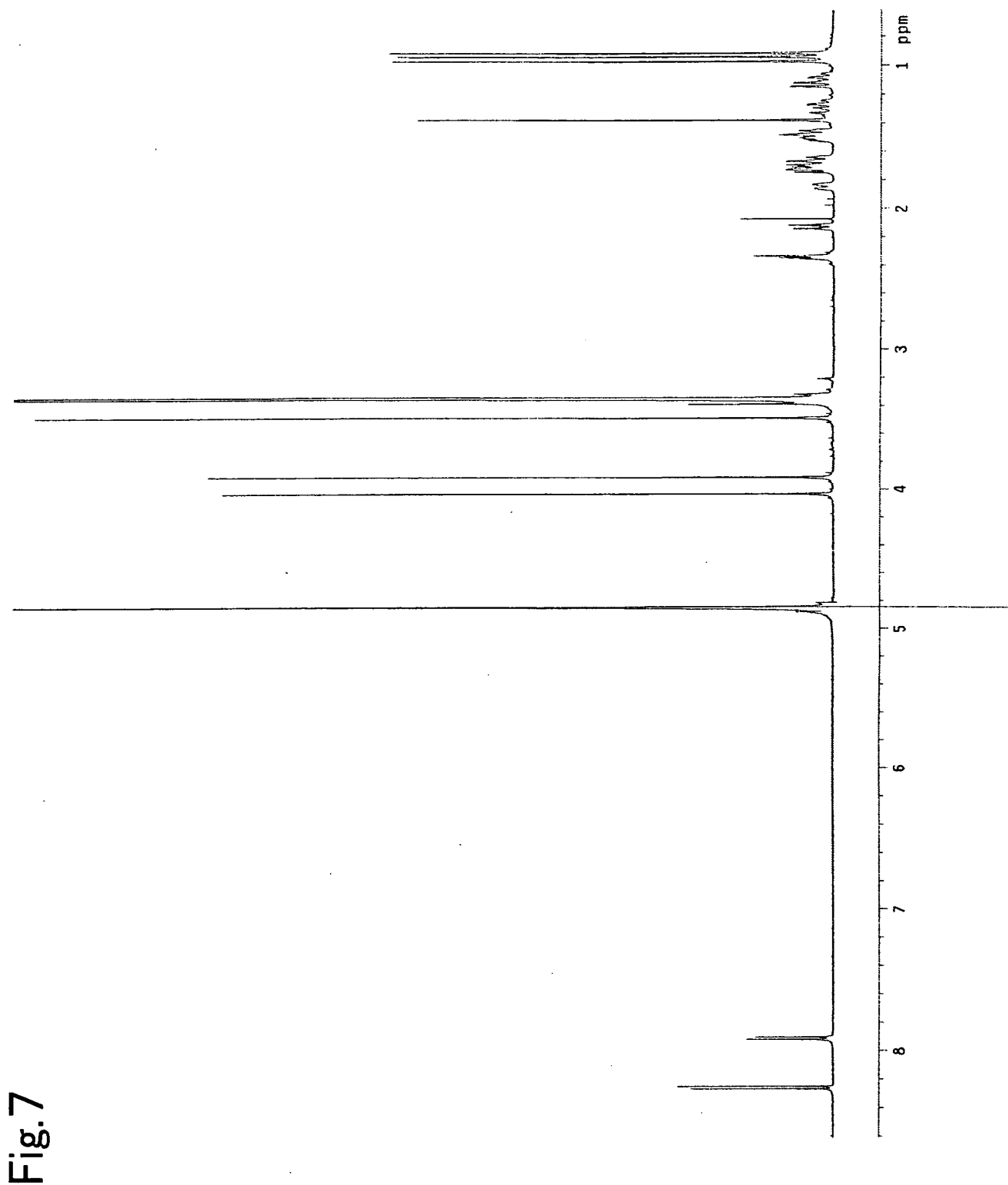


Fig. 8

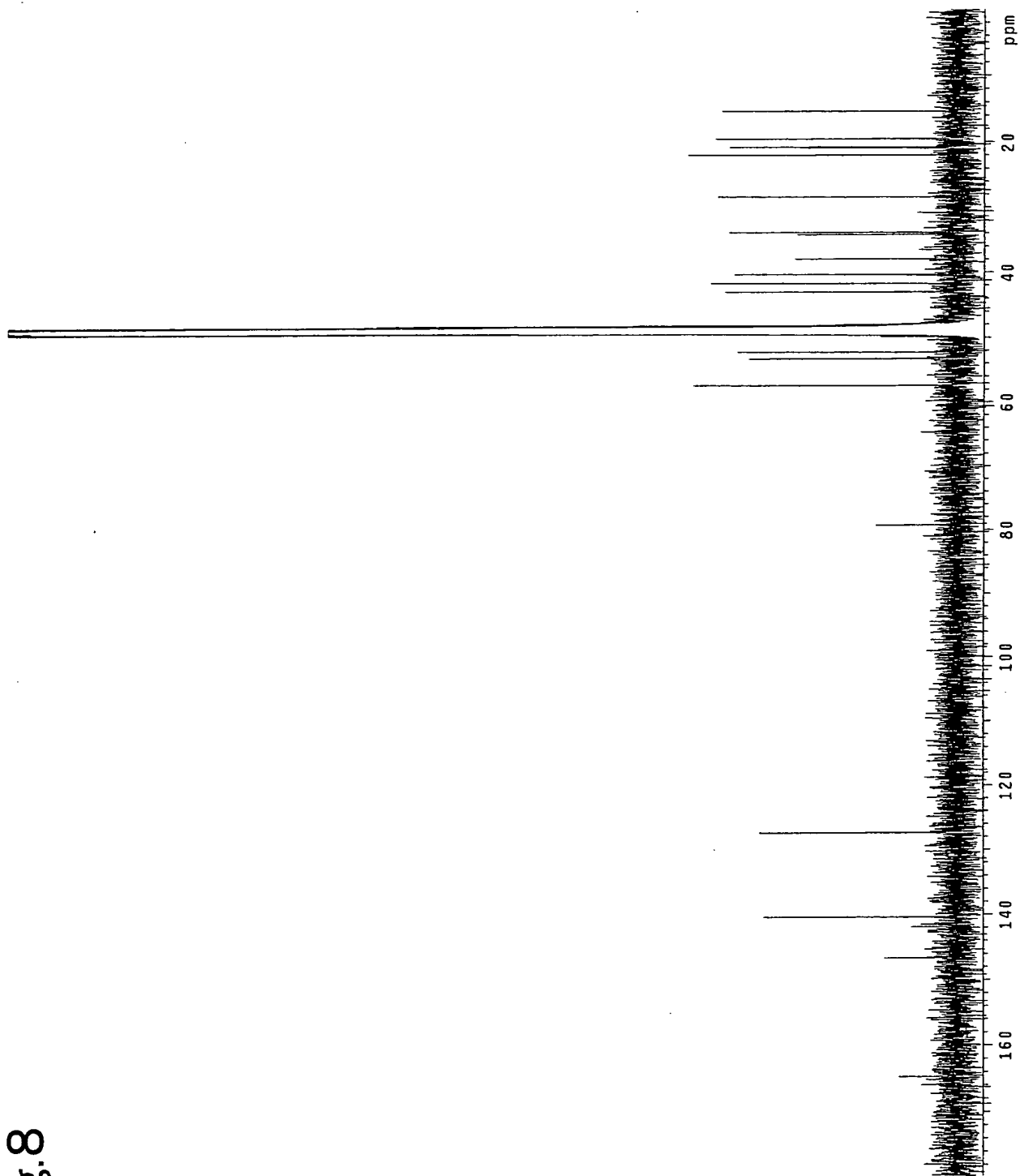
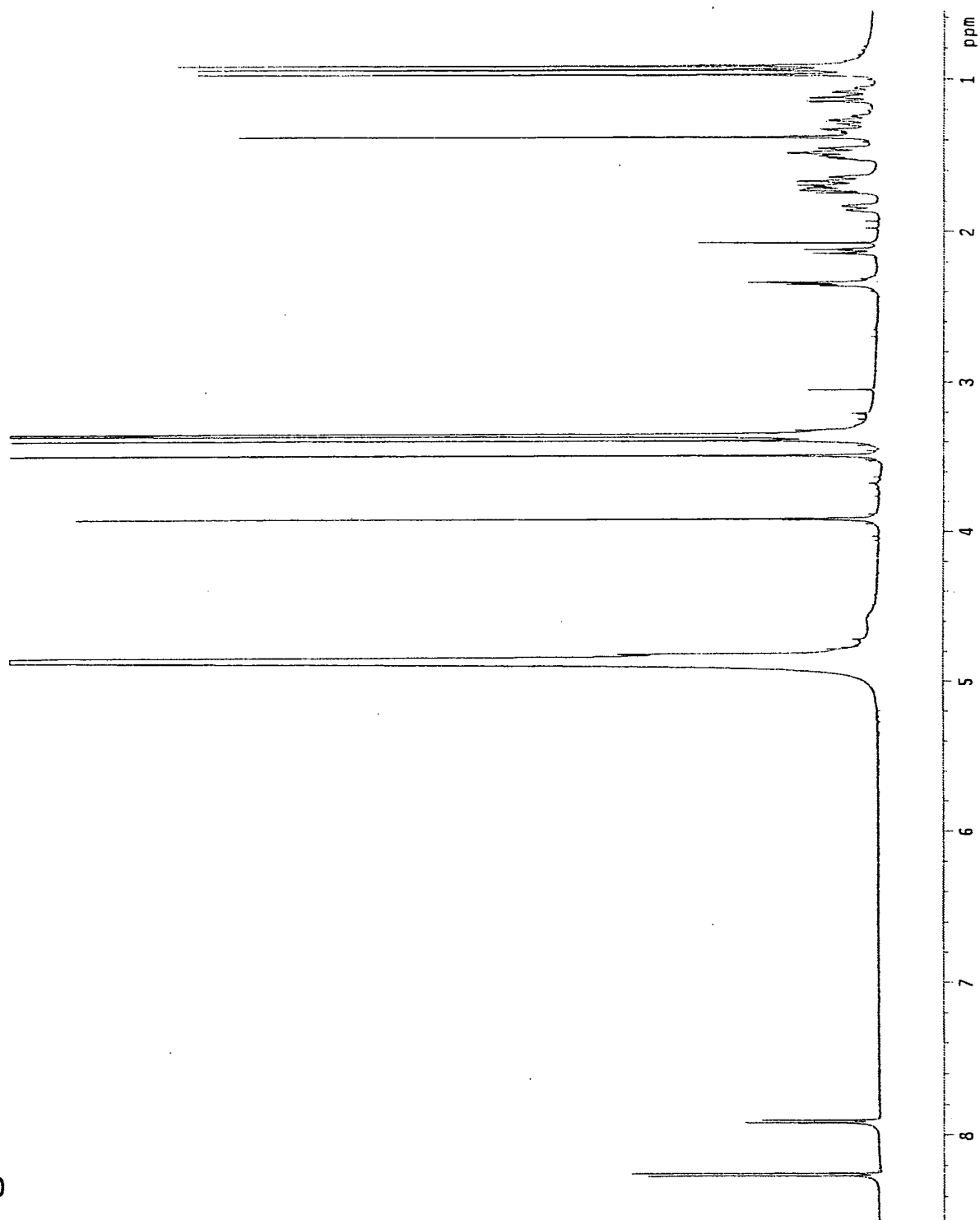
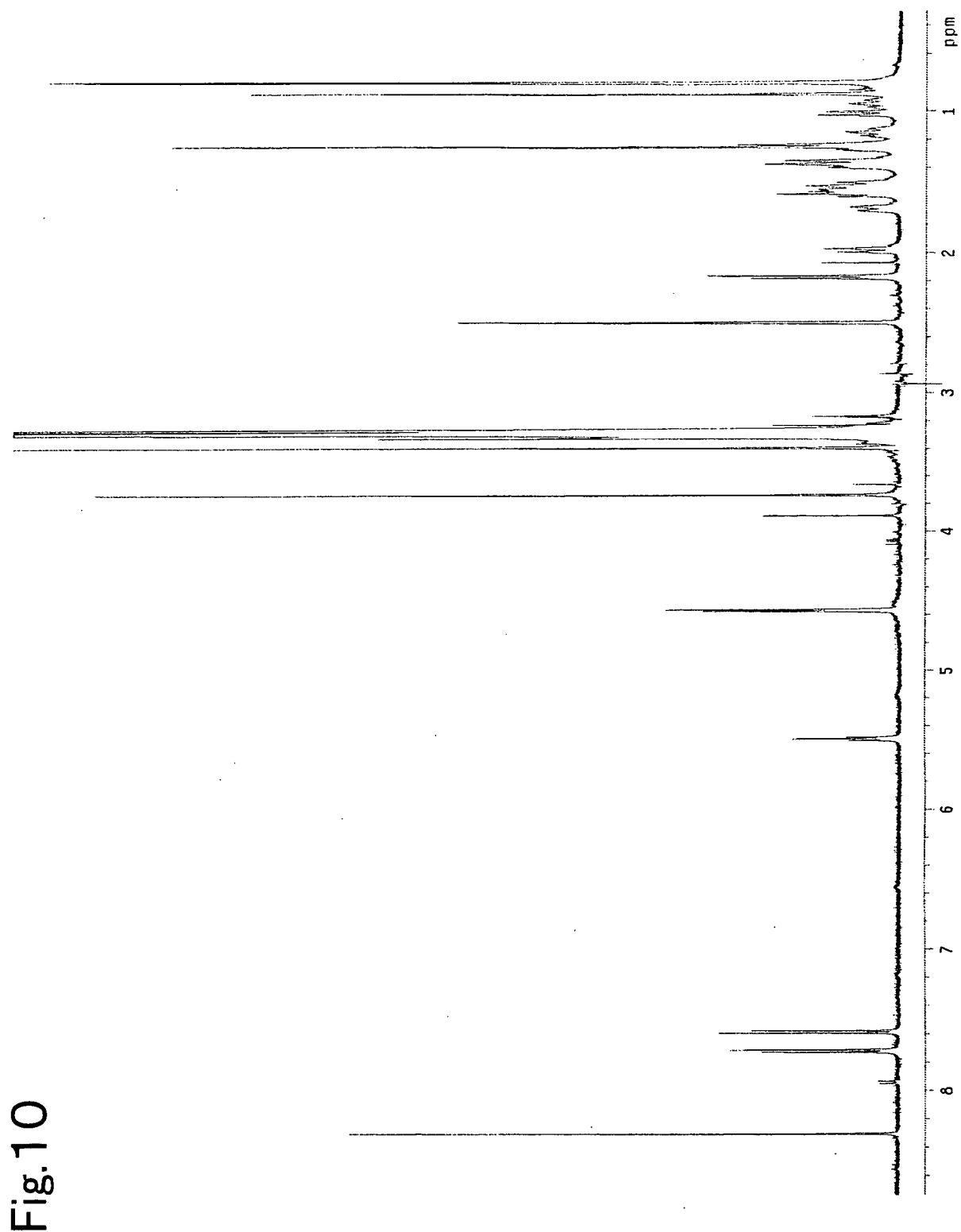
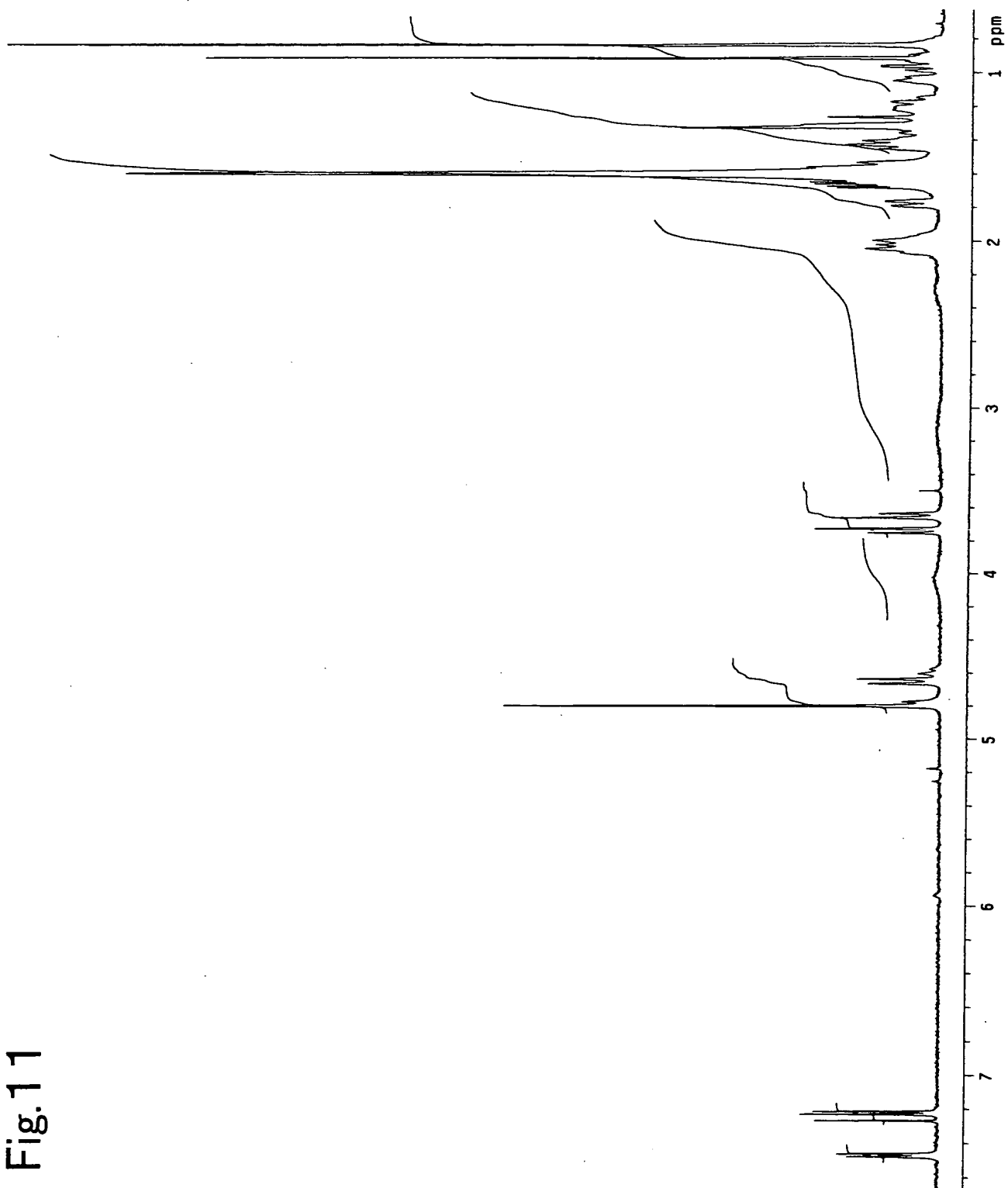


Fig. 9





Replacement Drawing



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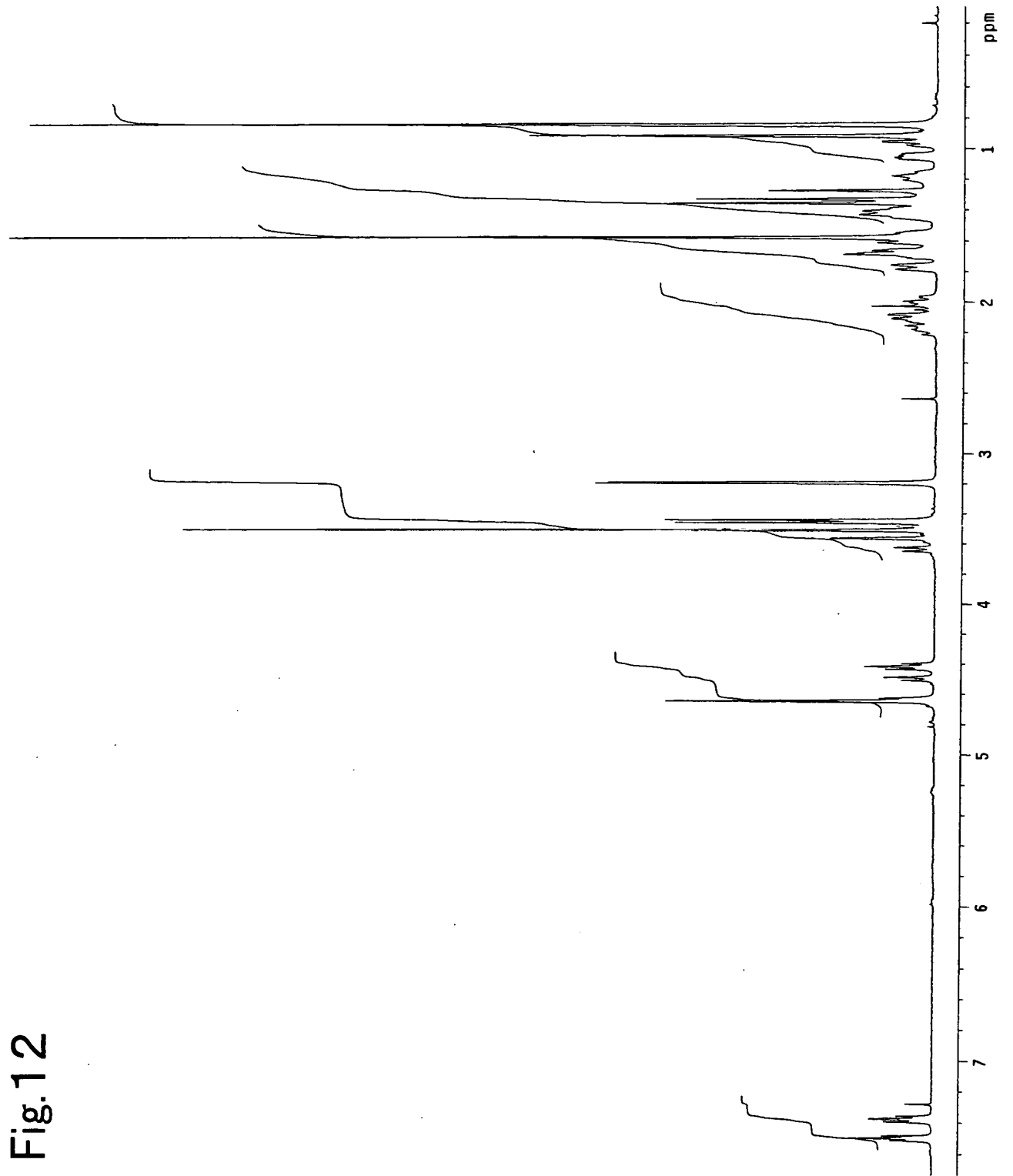


Fig.13



Fig.14

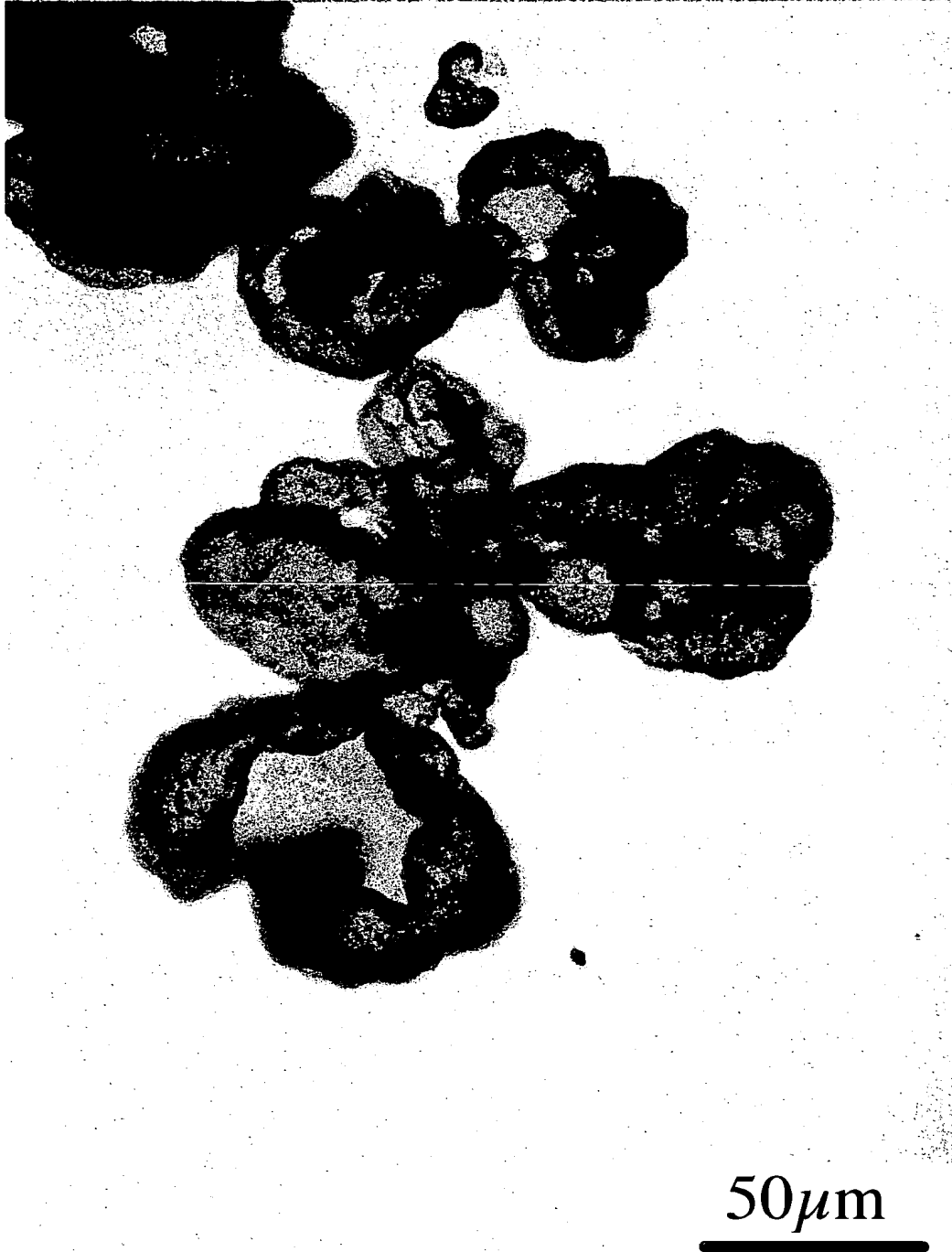
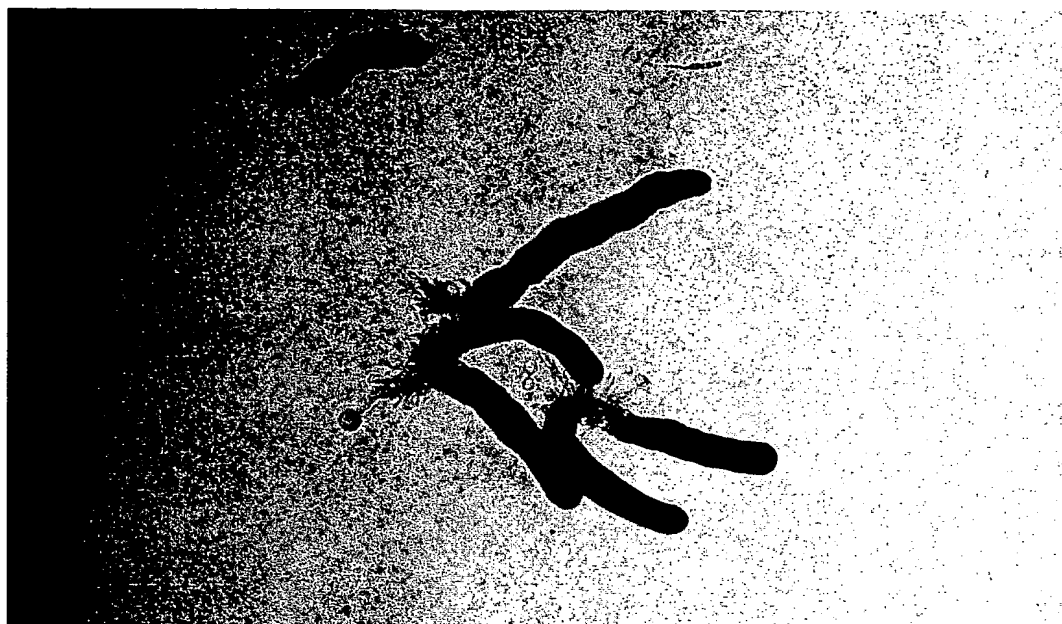
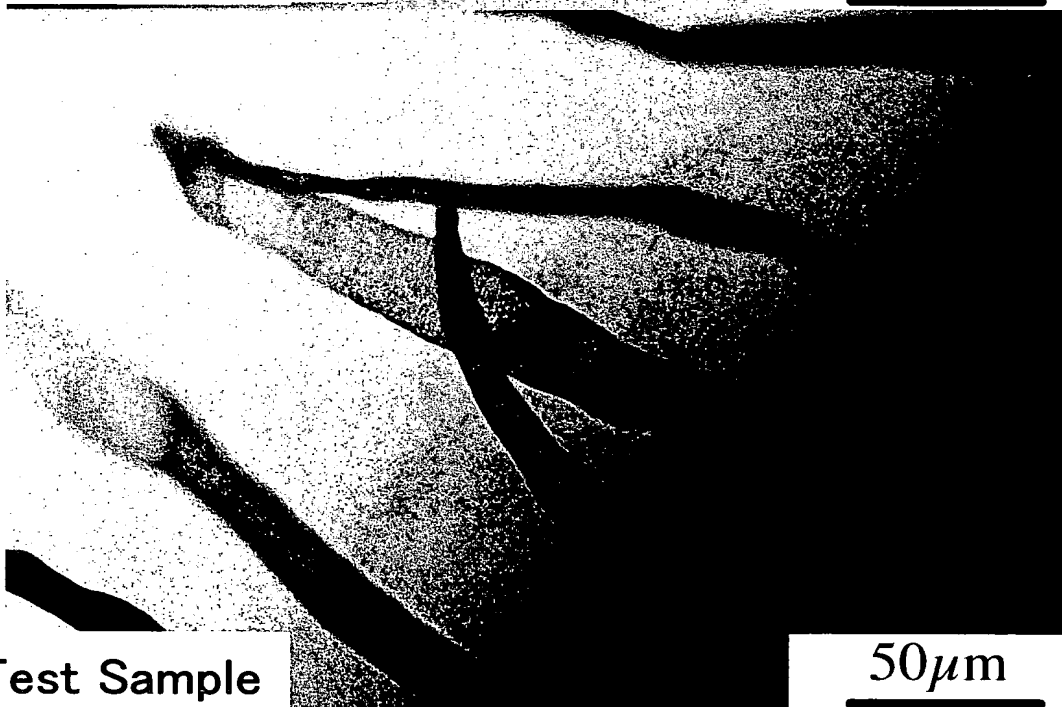


Fig.15



Control Sample

50 μ m



Test Sample

50 μ m

Fig.16

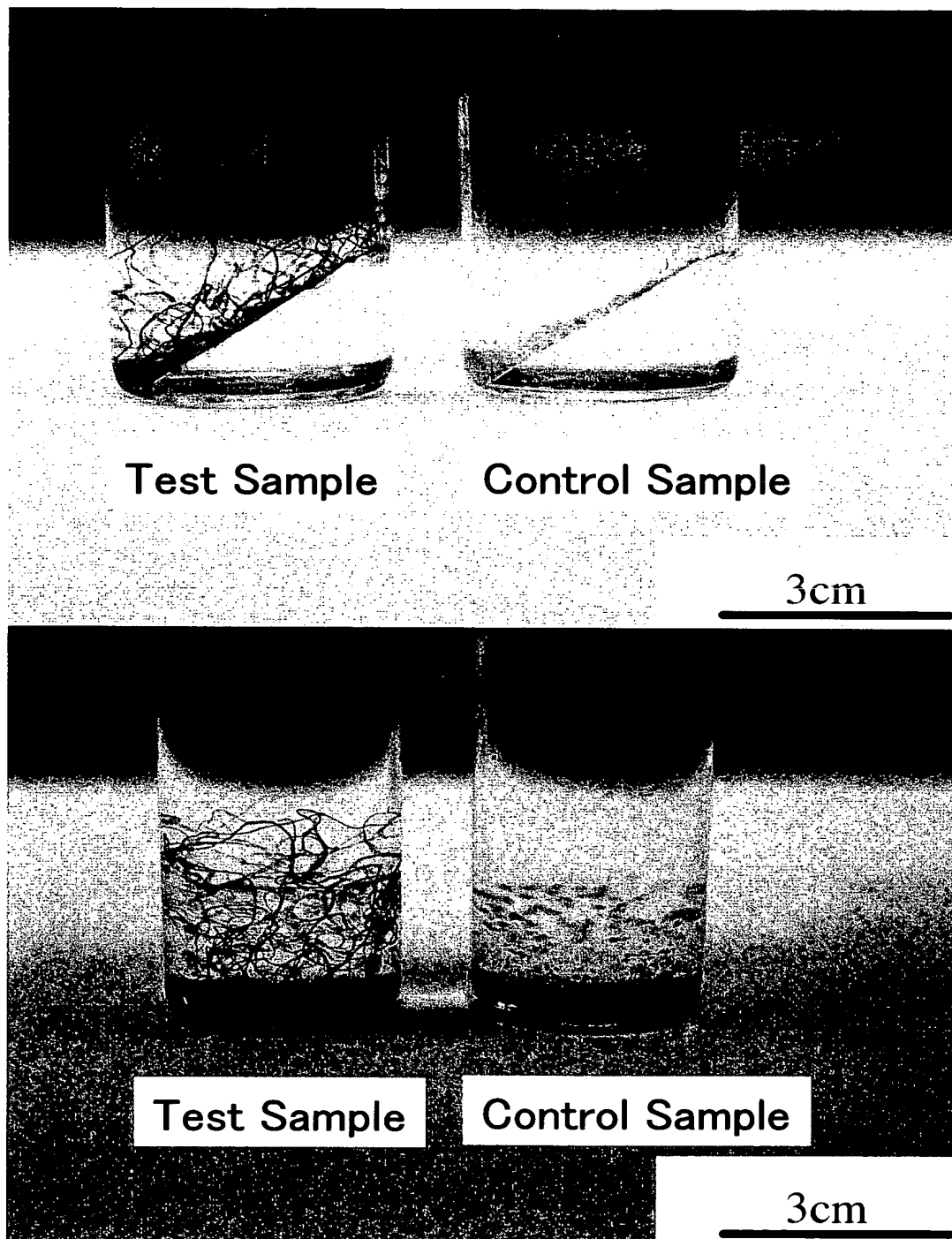
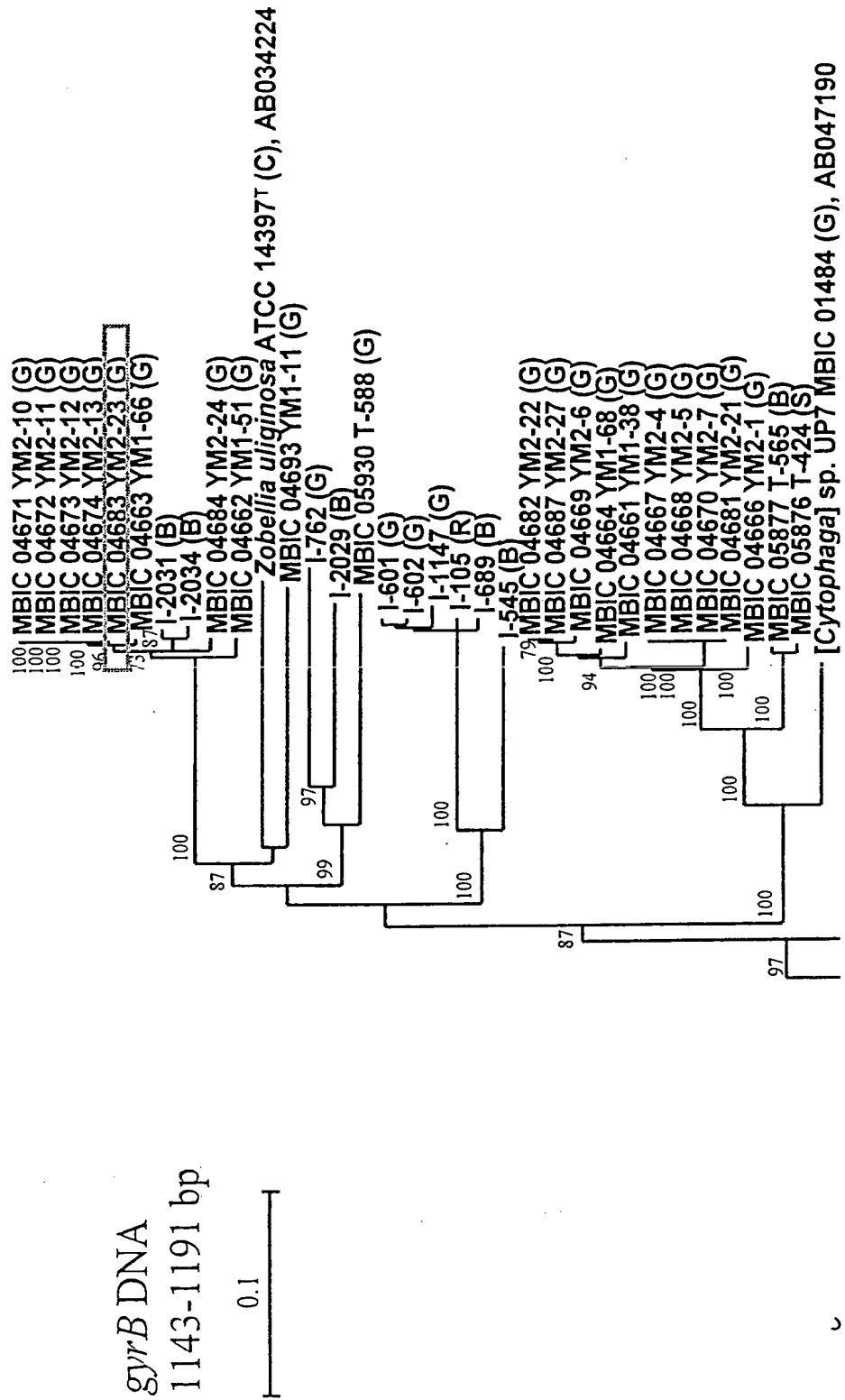
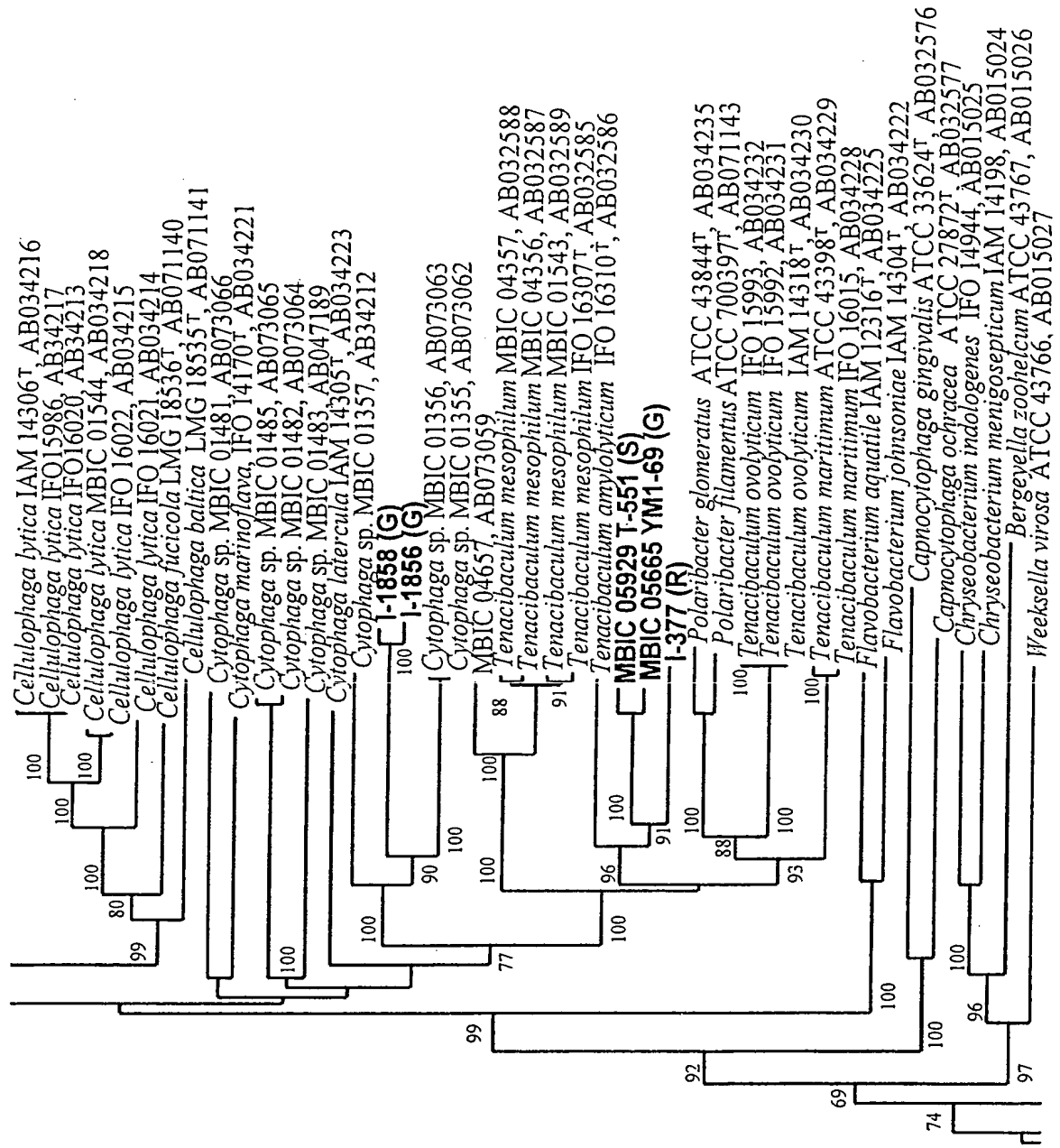


Fig.17



Fi 17



Phylogenetic tree showing the relationships between various bacterial strains based on the hsdR gene region. The tree is rooted at the bottom left. Bootstrap values are indicated at the nodes. The strains are grouped into several clusters, with some strains highlighted in bold. The tree is rooted at the bottom left.

Strains and their accession numbers (in parentheses):

- Cytophaga fermentans* IFO 15936^T, AB01531
- Pedobacter heparinus* IFO 12017^T (C), AB015035**
- Sphingobacterium spiritovorum* IAM 14210^T, AB015036
- Flammovirga aprica* ATCC 23126^T, AB034220
- Cytophaga hutchinsonii* IAM 12607^T, AB015037
- Cytophaga aurantiaca* IFO 16043, AB015038
- Flexibacter litoralis* ATCC 23117^T, AB034233
- MBIC 05879 T-561 (R)**
- Cyclobacterium marinum* LMG 13164 (C), AB071142**
- Cytophaga* sp. MBIC 01539 (S), AB073068**
- Cytophaga* sp. MBIC 01599 (S), AB073069**
- Bacteroides fragilis* ATCC 25285^T, AB073070
- Bacteroides vulgatus* IFO 14291^T, AB015029
- Persicobacter diffluens* IAM 14117^T, AB034219
- Flexibacter elegans* IFO 15055^T, AB032580
- Flexibacter flexilis* IFO 15060^T, AB032583
- Flavobacterium ferrugineum* IFO 14992^T, AB073076
- Chitinophaga pinensis* DSM 2588 (C), AB073077**
- Escherichia coli* K12, X04341

Bootstrap values at nodes: 70, 67, 100, 100, 100, 100, 100, 79, 100, 78, 90, 88, 100, 84.

Fig. 18

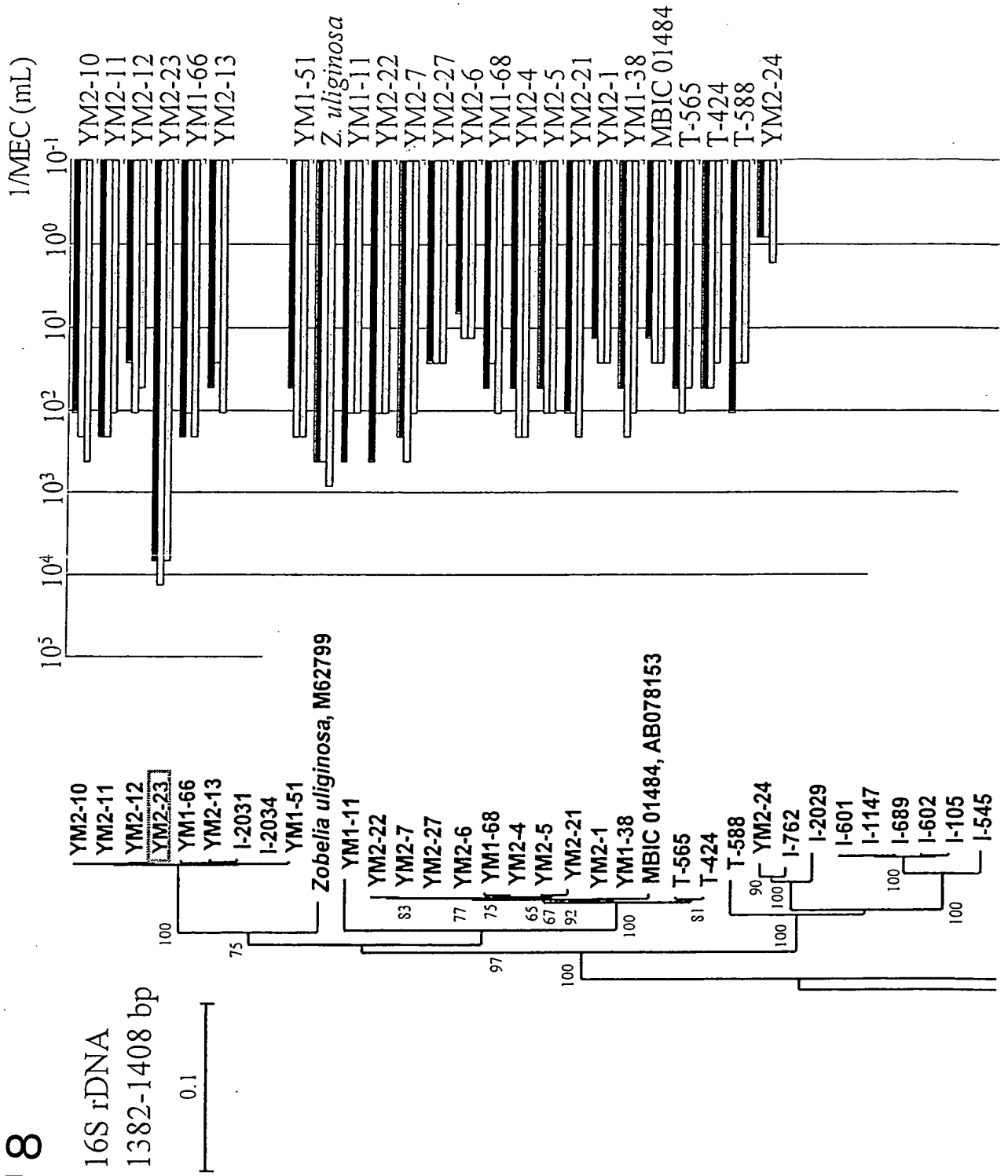


Fig.18

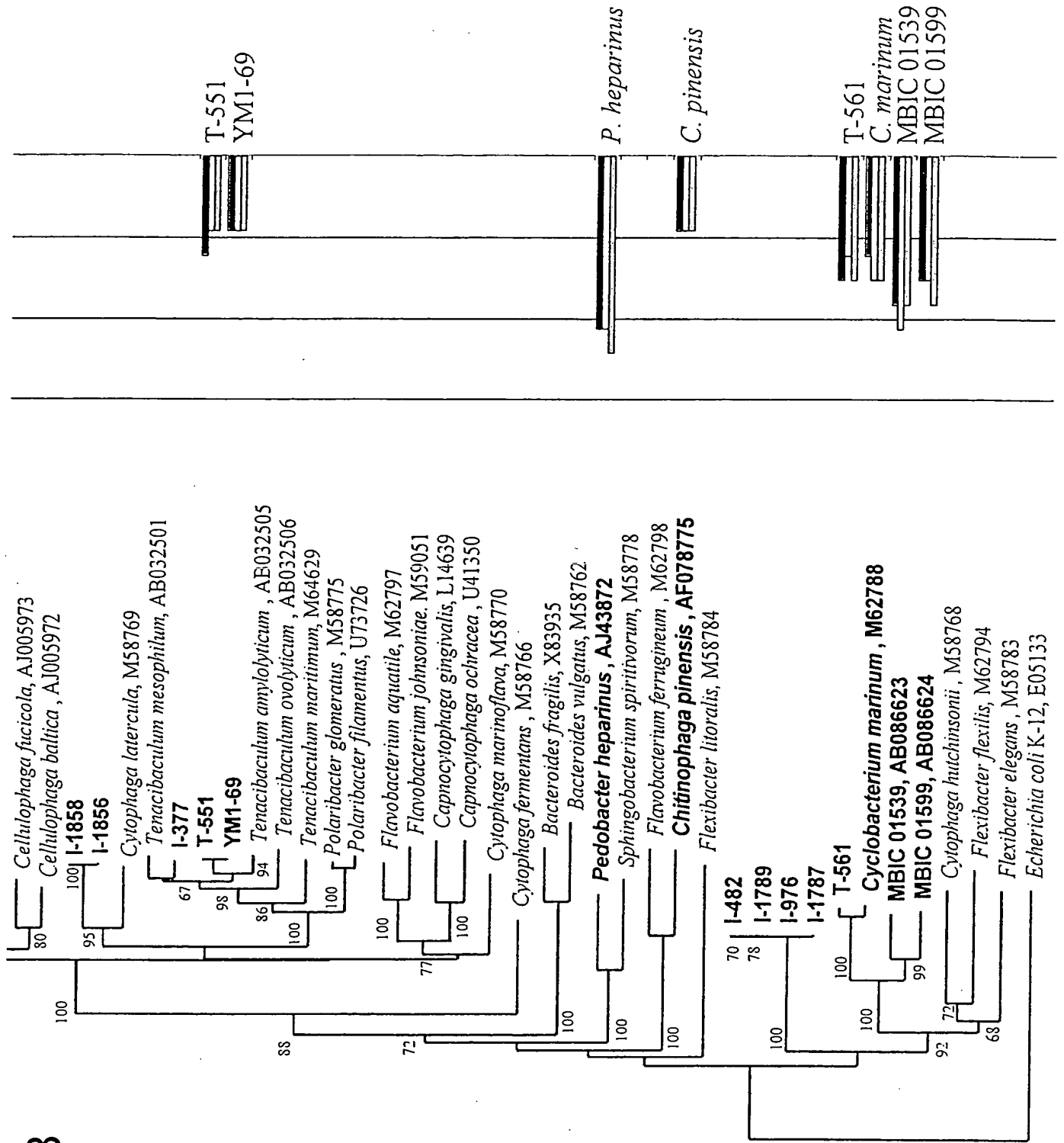


Fig. 19

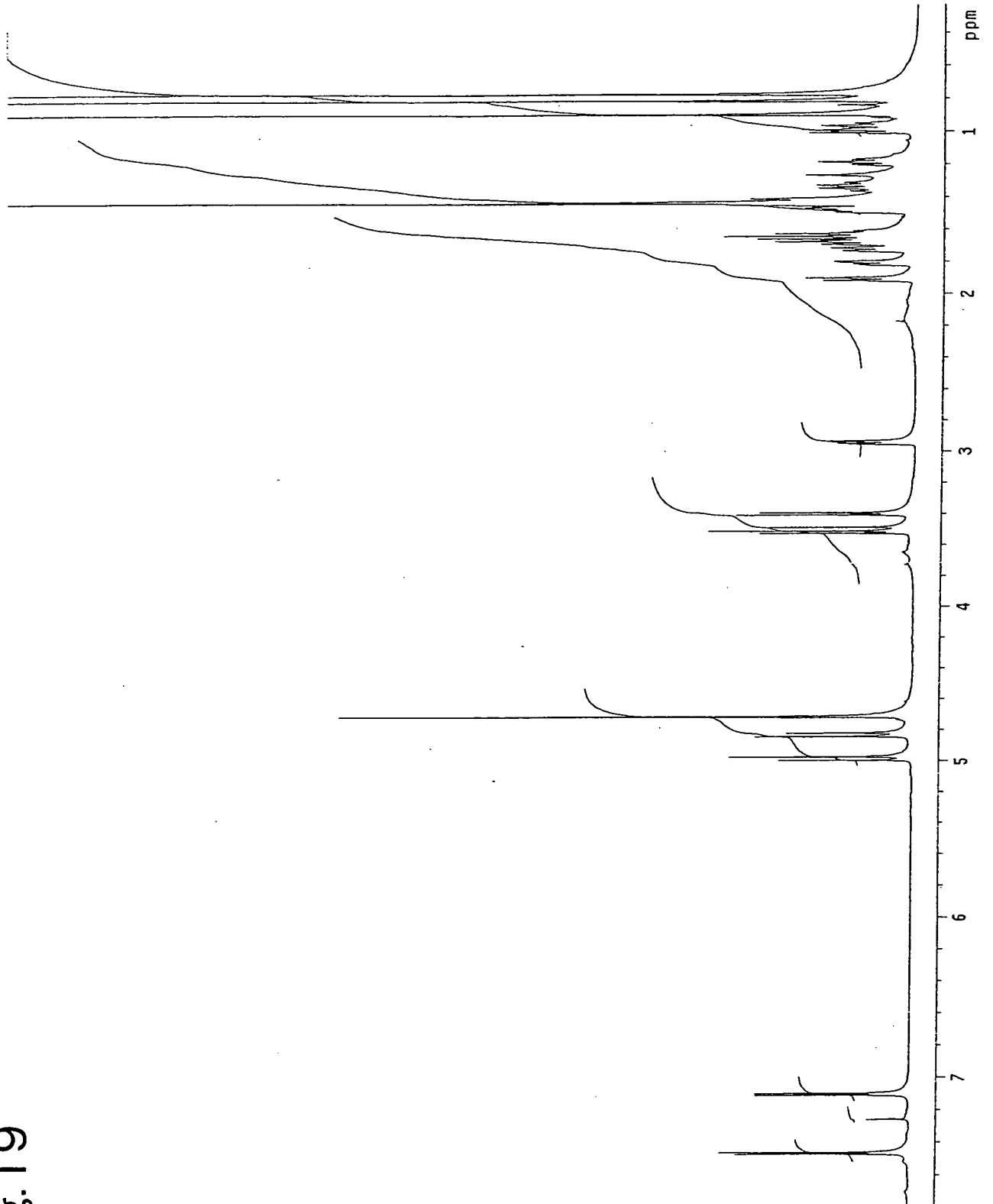


Fig.20

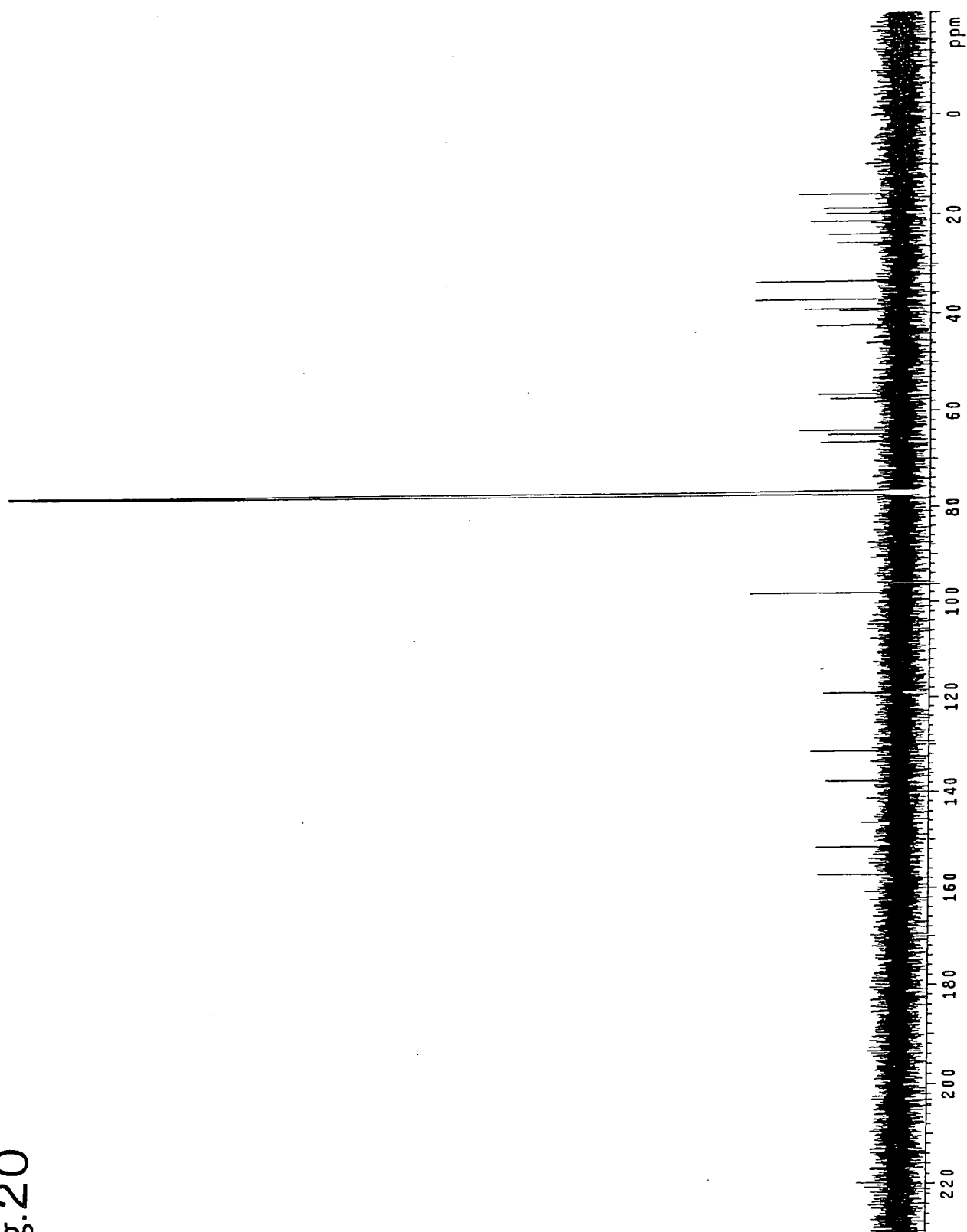


Fig.21

